

Figure 1

fraction: M L 21 22 23 24 25 26 27 28 29 30 31 32

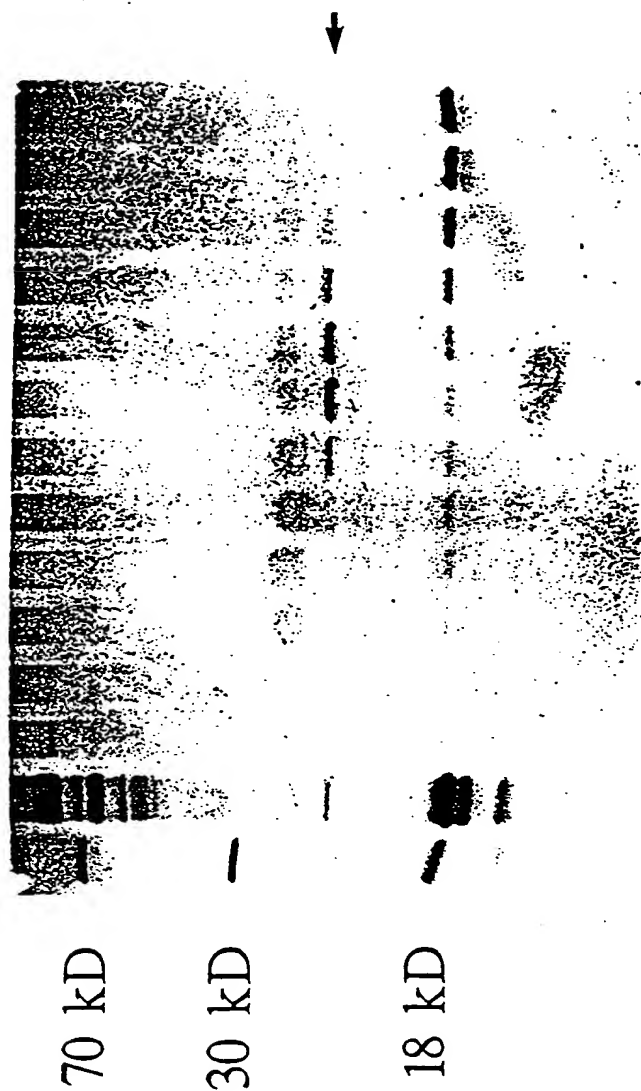


Figure 2a

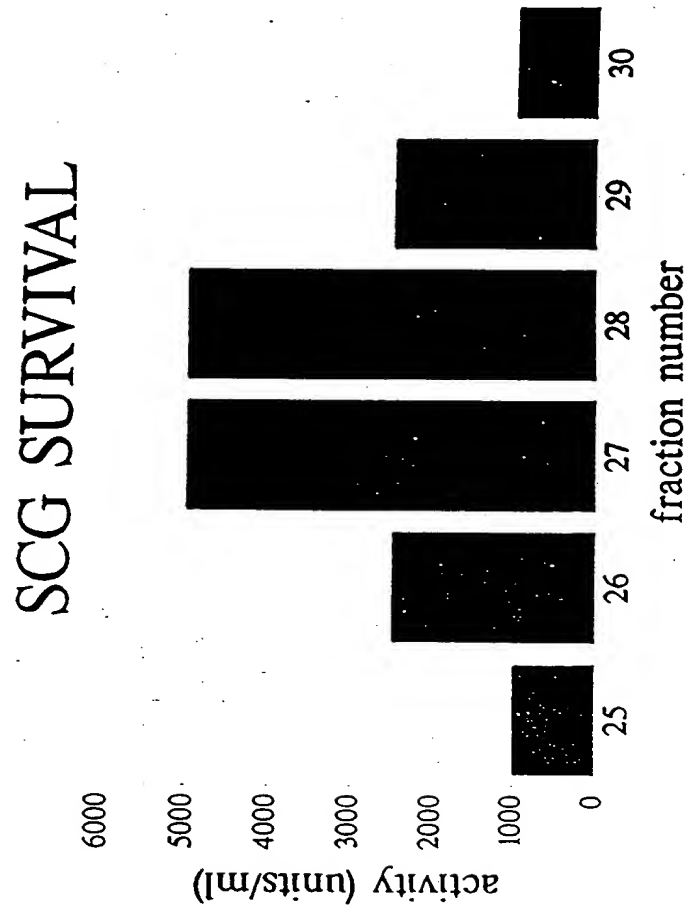


Figure 2b

Figure 3a NGF

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

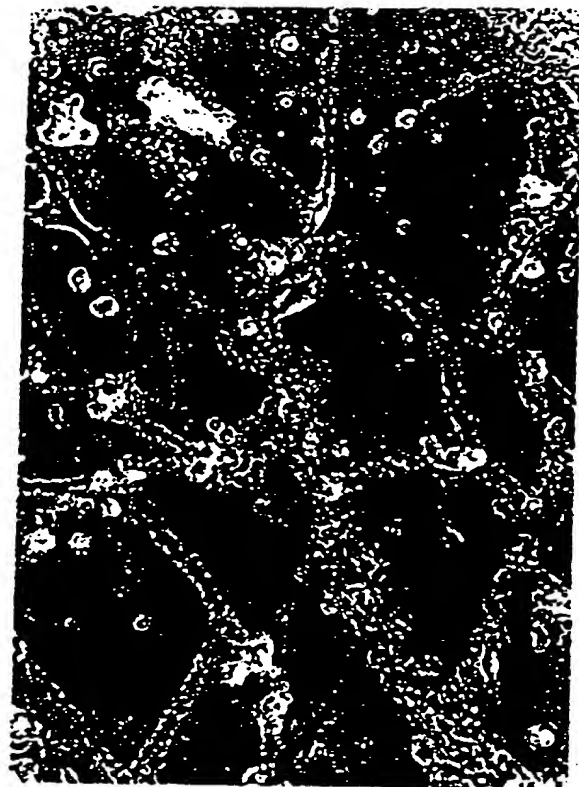
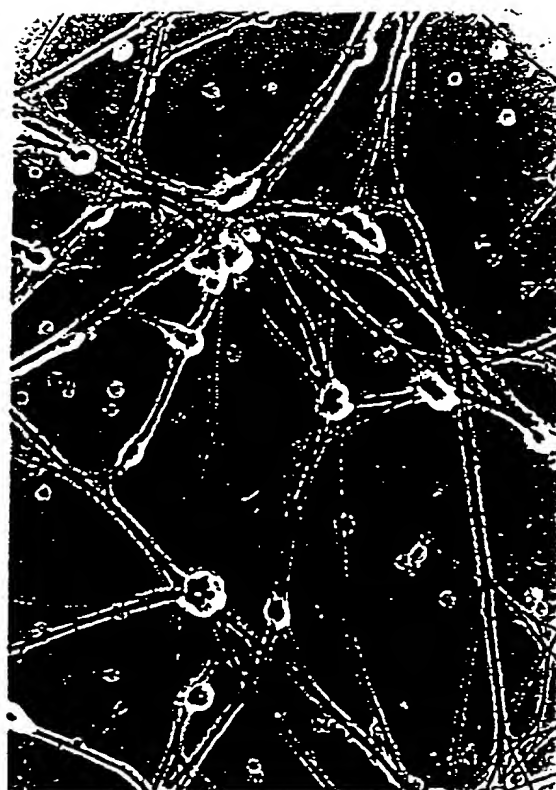


Figure 3c Anti-NGF  
+  
Neurturin



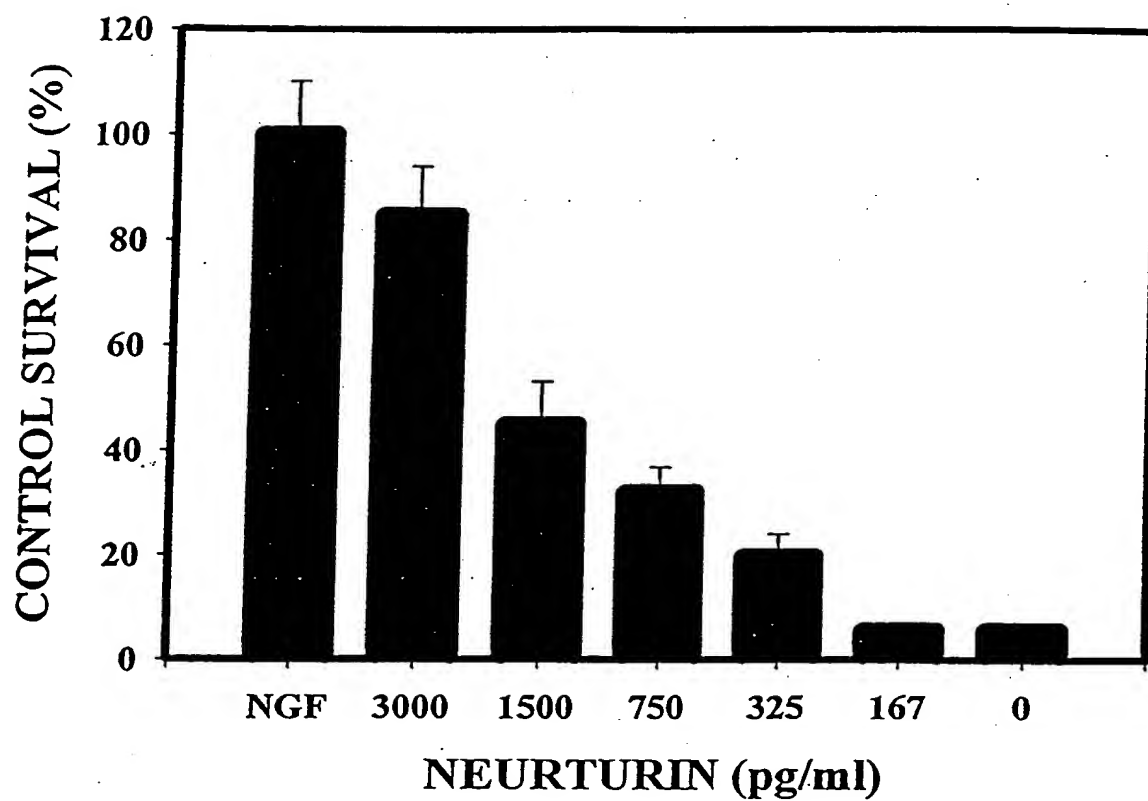


Figure 4

1	S	P	D	K	Q	H	A	V	L	P	R	R	E	R	N	R	Q	A	A	A	A	N	P	E	N	S	R	G	K	G	hGDNF	
1	S	P	D	K	Q	A	A	A	L	P	R	R	E	R	N	R	Q	A	A	A	A	S	P	E	N	S	R	G	K	G	mGDNF	
1	S	P	D	K	Q	A	A	A	L	P	R	R	E	R	N	R	Q	A	A	A	A	S	P	E	N	S	R	G	K	G	rGDNF	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hNTN	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	mNTN	
31	R	R	G	Q	R	G	K	N	R	G	C	V	L	T	A	I	H	L	N	V	T	D	L	G	L	G	Y	E	T	K	hGDNF	
31	R	R	G	Q	R	G	K	N	R	G	C	V	L	T	A	I	H	L	N	V	T	D	L	G	L	G	Y	E	T	K	mGDNF	
31	R	R	G	Q	R	G	K	N	R	G	C	V	L	T	A	I	H	L	N	V	T	D	L	G	L	G	Y	E	T	K	rGDNF	
1	-	-	-	-	A	R	L	G	A	R	P	C	G	L	R	E	L	E	V	R	V	S	E	L	G	L	G	Y	A	S	D	hNTN
1	-	-	-	-	P	G	A	R	P	C	G	L	R	E	L	E	V	R	V	S	E	L	G	L	G	Y	T	S	D	-	-	mNTN
61	E	E	L	I	F	R	Y	C	S	G	S	C	D	A	A	E	T	T	Y	D	K	I	L	K	N	L	S	R	N	R	hGDNF	
61	E	E	L	I	F	R	Y	C	S	G	S	C	E	S	A	E	T	M	Y	D	K	I	L	K	N	L	S	R	S	R	mGDNF	
61	E	E	L	I	F	R	Y	C	S	G	S	C	E	A	A	E	T	M	Y	D	K	I	L	K	N	L	S	R	S	R	rGDNF	
28	E	T	V	L	F	R	Y	C	A	G	A	C	E	A	A	A	R	V	Y	D	L	G	L	R	R	L	R	Q	R	R	hNTN	
26	E	T	V	L	F	R	Y	C	A	G	A	C	E	A	A	I	R	I	Y	D	L	G	L	R	R	L	R	Q	R	R	mNTN	
91	R	L	V	S	D	K	V	-	G	Q	A	C	C	R	P	I	A	F	D	D	D	L	S	F	L	D	D	N	L	V	hGDNF	
91	R	L	T	S	D	K	V	-	G	Q	A	C	C	R	P	V	A	F	D	D	D	L	S	F	L	D	D	N	L	V	mGDNF	
91	R	L	T	S	D	K	V	-	G	Q	A	C	C	R	P	V	A	F	D	D	D	L	S	F	L	D	D	S	L	V	rGDNF	
58	R	L	R	R	E	R	V	R	A	Q	P	C	C	R	P	T	A	Y	E	D	E	V	S	F	L	D	A	H	S	R	hNTN	
56	R	V	R	R	E	R	A	R	A	H	P	C	C	R	P	T	A	Y	E	D	E	V	S	F	L	D	V	H	S	R	mNTN	
120	Y	H	I	L	R	K	H	S	A	K	R	C	G	C	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hGDNF	
120	Y	H	I	L	R	K	H	S	A	K	R	C	G	C	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	mGDNF	
120	Y	H	I	L	R	K	H	S	A	K	R	C	G	C	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	rGDNF	
88	Y	H	T	V	H	E	L	S	A	R	E	C	A	C	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hNTN	
86	Y	H	T	L	Q	E	L	S	A	R	E	C	A	C	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	mNTN	

Figure 5



RT-PCR Analysis of Neurturin and GDNF

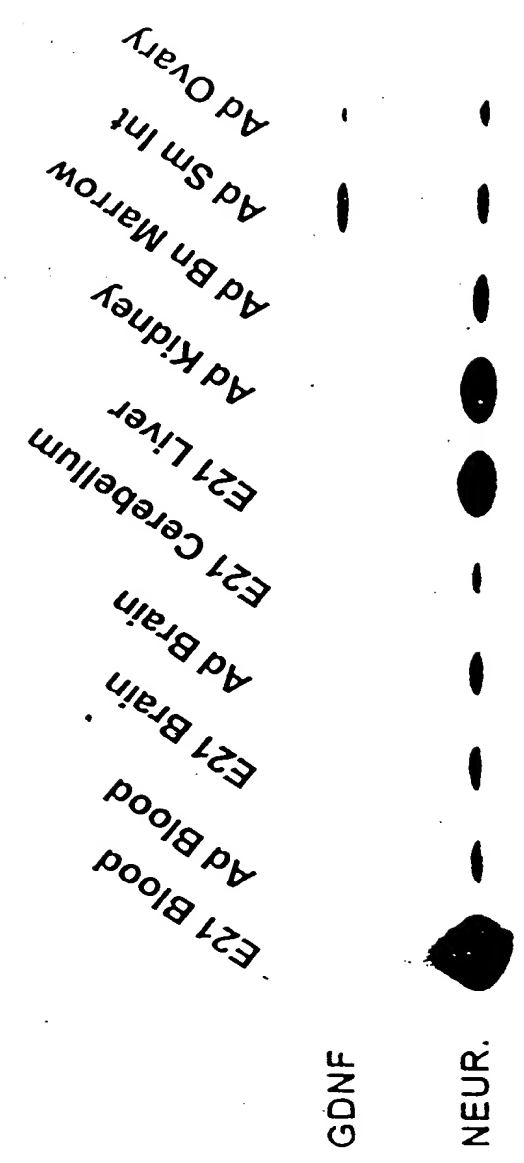


Figure 6

ATGCAGCGCTGGAAGGCGGCGGCCTTGGCCTCAGTGCTCTGCAGCTCCGTGCTGTCCATC 60  
Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser Val Leu Ser Ile  
 TGGATGTGTGAGAGGGCCTGCTTCTCAGCCACCGCCTCGGACCTGCGCTGGTCCCCTG 120  
Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro Ala Leu Val Pro Leu  
 CACCGCCTGCCTCGAACCCTGGACGCCCCGATTGCCCGCCTGGCCAGT<sup>+</sup>ACCGTGCACTC 180  
His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu  
 CTGCAGGGGGCCCCGGATGCGATGGAGCTGCGCGAGCTGACGCCCTGGGCTGGGCGGCCCC 240  
Leu Gln Gly Ala Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro  
 CCAGGTCCGCGCCGTGCGGCGGGGCCCCGGCGGCGGCGCGCGCTGCGCGGTTGGGGGCG 300  
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala Arg Leu Gly Ala  
 CGGCCTTGCGGGCTGCGCGAGCTGGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACGCG 360  
Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala  
 TCCGACGAGACGGTGCTGTTCCGCTACTGCGCAGGCGCCTGCGAGGCTGCCGCGCGCGTC 420  
Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val  
 TACGACCTCGGGCTGCGACGACTGCGCCAGCGGCGGCGCCTGCGGCGGGAGCGGGTGCGC 480  
Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg  
 GCGCAGCCCTGCTGCCGCCCGACGGCCTACGAGGACGAGGTGTCCTTCCTGGACGCGCAC 540  
Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His  
 AGCCGCTACCACACGGTGACGAGCTGTCGGCGCGCGAGTGCGCCTGCGTGTGA 594  
Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val

Figure 7

ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTGCTCATCTGCAGCTCCCTGCTATCTGTC 60  
Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser Leu Leu Ser Val  
 TGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGGGACCCGCGCTTGCCCCGCTA 120  
Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro Ala Leu Ala Pro Leu  
 CGACGCCCTCCACGCACCCTGGACGCCCGCATCGCCCGCCTGGCCCAGTATCGCGCTCTG 180  
Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu  
 CTCCAGGGCGCCCCGACGCGGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCCGCATC 240  
Leu Gln Gly Ala Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile  
 CCGGGACCGCGCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGGGCTCGGCCT 300  
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro Gly Ala Arg Pro  
 TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTACACGTCGGAT 360  
Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Thr Ser Asp  
 GAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGGCGGCCATCCGCATCTACGAC 420  
Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp  
 CTGGGCCTTCGGCGCCTGCGCCAGCGGAGGCGCGTGCGCAGAGAGCGGGCGCGGGCGCAC 480  
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His  
 CCGTGTTGTCGCCCCGACGGCCTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGC 540  
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg  
 TACCACACGCTGCAAGAGCTGTGCGCGCGGGAGTGCGCGTGCGTGTGA 588  
Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val

Figure 8

GGAGGGAGAGCGCGCGGTGGTTTCGTCCGTGTGCCCCGCGCCCGGCGC	-301
TCCTCGCGTGGCCCCGCGTCCTGAGCGCGCTCCAGCCTCCCACGCGCGCC	-251
ACCCCGGGGTTCAGTGAAGCCGCGAGCCCGGGGAAGACAGAGAAAGAGA	-201
GGCCAGGGGGGGAACCCCATGGCCCCGGCCCGTGTCCCGCACCCCTGTGCGG	-151
TGGCCTCCTCCGGCACGGGGTCCCCGGGTGCGCTCCGGTCCCCGCGATCC	-101
GGATGGCGCACGCAGTGGCTGGGGCCGGGCCGGGCTCGGGTGGTCGGAGG	-51
AGTCAACCACTGACGGGTCACTCTGGAGCCCGTGGCAGGCCGAGGCCAGG	-1
ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTGCTCATCTGCAGCTCCCT	50
<u>GCTATCTGTCTGGATGTGCCAGGAGGGTCTGCTCTTGGGCCACCGCCTGG</u>	100
<u>GACCCGCGCTTGCCCCGCTACGACGCCCTCCACGCACCCCTGGAAGCCCGC</u>	150
<u>ATCGCCCGCCTGGCCAGTATGCGCTCTGCTCCAGGGCGCCCCGAAGC</u>	200
<u>GGTGGAGCTTCGAGAACTTTCTCCCTGGGCTGCCCGCATCCCGGGACCGC</u>	250
<u>GCCGTGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGGGCTCGGCCT</u>	300
<u>TGTGGGCTGCGGAGCTCGAGGTGCGCGTGAGCGAGCTGGGCCTGGGCTA</u>	350
<u>CACGTGGATGAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCGAGG</u>	400
<u>CGGCCATCCGCATCTACGACCTGGGCCTTCGGGCGCTGCGCCAGCGGAGG</u>	450
<u>CGCGTGCGCAGAGAGCGGGCGCGGGCGCACCCGTGTTGTGCCCCGACGGC</u>	500
<u>CTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGCTACCACAGC</u>	550
<u>TGCAAGAGCTGTGCGCGCGGGAGTGCGCGTGCGTGTGATGCTACCTCAG</u>	600
CCCCCGACCTGCGAAAGGGCCCTCCCTGCCGACCCTCGCTGAGAACTGA	650
CTTCACATAAAGTGTGGGAACTCCC	675

Figure 9

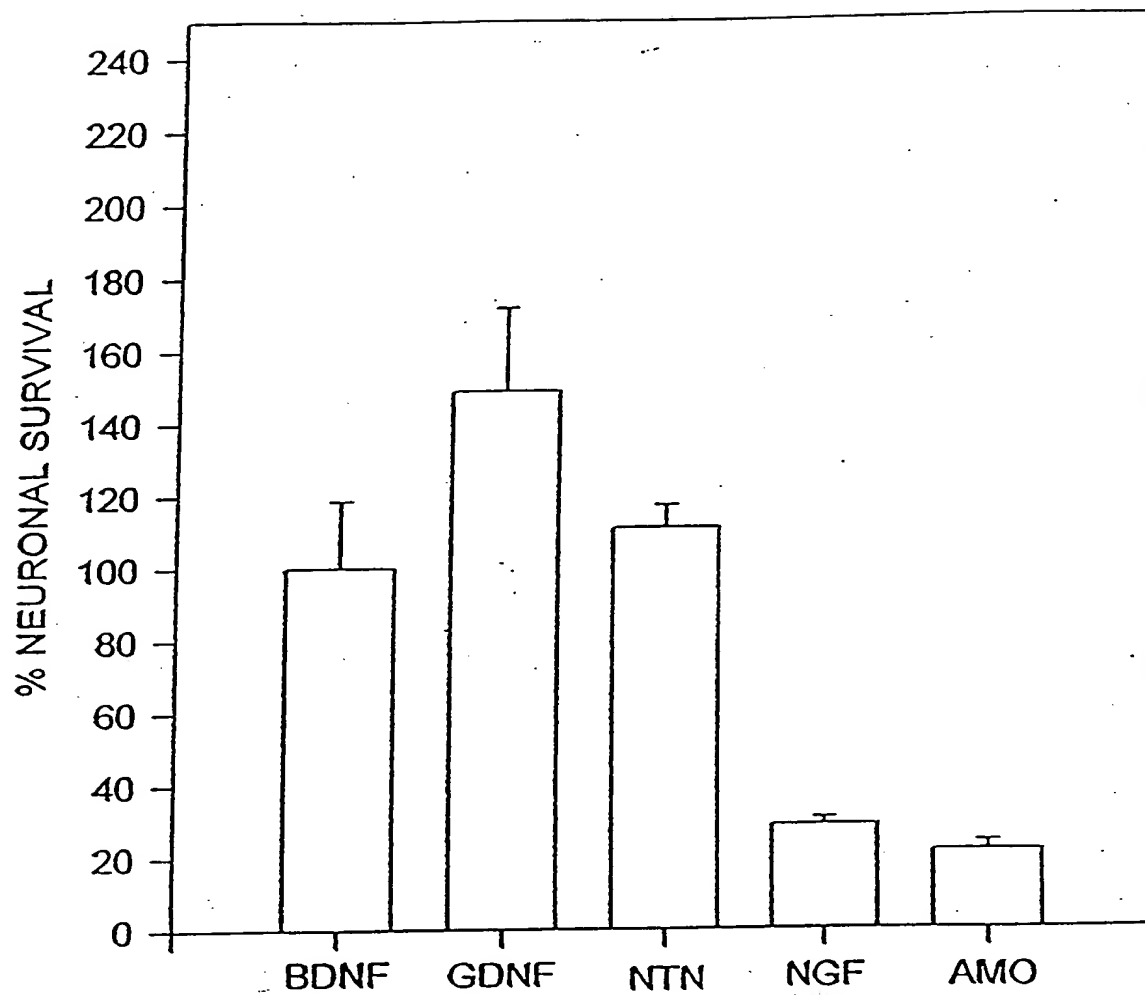


Figure 10

GAGGGACCTGGACGCCCCATCAGGGTAAGAATTCCTGGGGGCCTCCCGACTCCCCAATTC	60
Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro Thr Pro Gln Phe	20
CTTCTCTCAAAGCCCTCACTTTGCCTTACAATCCTACTCTACCTTGCACTAGGTAACAAC	120
Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu Leu Tyr Leu Ala Leu Gly Asn Asn	40
CATGTCCGTCTTCCAAGAGCCCTTGGCTGGTTCATGCCGACTGTGGAGCCTGACCCTACCA	180
His Val Arg Leu Pro Arg Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro	60
GTGGCTGAGCTGGGCCTGGGCTATGCCTCGGAGGAGAAGGTCATCTTCGATACTGTGCT	240
Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala	80
GGCAGCTGTCCCCAAGAGGCCCGTACCCAGCACAGTCTGGTACTGGCCCGGCTTCGAGGG	300
Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly	100
CGGGGTGAGCCCCATGGCCGACCCTGCTGCCAGCCCACCAGCTATGCTGATGTGACCTTC	360
Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe	120
CTTGATGATCAGCACCATTTGGCAGCAGCTGCCTCAGCTCTCAGCTGCAGCTTGTGGCTGT	420
Leu Asp Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys	140
GGTGGCTGAAGGAGGCCAGTCTGGTGTCTCAGAATCACAAGCATGAGACAGGCTGGGCTT	480
Gly Gly	142
TGAAAGGCTCAGGTGACATTACTAGAAATTTGCATAGGTAAAGATAAGAAGGGAAAGGAC	540
CAGG	544

Figure 11

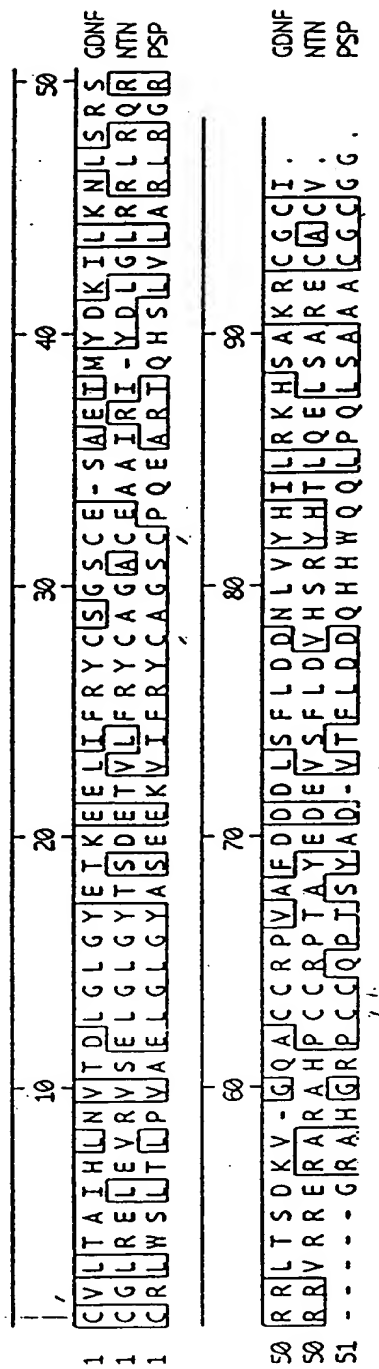


Figure 12

CCTCAGAGGAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACC 62  
 Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr 20

CAGCACAGTCTGGTGCTGGCCCCGTCTTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGC 122  
 Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys 40

TGCCAGCCCACCAGCTATGCTGATGTGACCTTCCTTGATGACCACCACCATTGGCAGCAG 182  
 Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln 60

CTGCCTCAGCTCTCAGCCGCAGCTTGTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCT 242  
 Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly 73

CTCAGAATCACAAGCAAGAGGCAGCCTTTGAAAGGCTCAGGTGACGTTATTAGAAACTTG 302

CATAGGAGAAGATTAAGAAGAGAAAGGGGACCTG 336

Figure 13



TGCCGGCTGTGGAGCCTGACCCTACCAGTGGCTGAGCTTGGCCTGGGCTATGCCTCAGAG	60
Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu	20
GAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACCCAGCAC	120
Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His	40
AGTCTGGTGCTGGCCCGTCTTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGCTGCCAG	180
Ser Leu Val Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln	60
CCCACCAGCTATGCTGATGTGACCTTCCTTGATGACCACCACCATTGGCAGCAGCTGCCT	240
Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro	80
CAGCTCTCAGCCGCAGCTTGTTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCTCTCAGA	300
Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly	91
ATCACAAGCAAGAGGCAGCCTTTGAAAGGCTCAGGTGACGTTATTAGAACTTGTCATAGG	360
AGAAGATTAAGAAGAGAAAGGGGACCTGATT	391

Figure 14



	10	20	30	
1	A L A G S C R L W S L T L P V A E E L G L G Y A S E E K V I F			mPSP
1	A L P G L C R L W S L T L P V A E E L G L G Y A S E E K I I F			rPSP
1	A L S G P C Q L W S L T L S V A E E L G L G Y A S E E K V I F			hPSP
31	R Y C A G S C P Q E A R T Q H S L V L A R L R G R G R A H G	50	60	mPSP
31	R Y C A G S C P Q E V R T Q H S L V L A R L R G Q Q G R A H G			rPSP
31	R Y C A G S C P R G A R T Q H G L A L A R L Q Q G Q G R A H G			hPSP
61	R P C C C Q P T S Y A D V T F L D D D Q H H W Q Q L P Q L S A A	80	90	mPSP
61	R P C C C Q P T S Y A D V T F L D D D Q H H W Q Q L P Q L S A A			rPSP
61	G P C C C R P T R Y T D V A F L D D D R H R W Q Q L P Q L S A A			hPSP
91	A C G C C G G G			rPSP
91	A C G C C G G G			rPSP
91	A C G C C G G G			hPSP

## Figure 15B

EO	D	GROWTH	0:	FACTOR	SEQUENCE
50		TGFβ1			CCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYINSLDT-----QYSKVLALYNQHNPGASAA-PCCV--POALEPLPIVYVGRKPKV--EQLSNMIVRSCKCS
51		TGFβ2			CCLRPLYIDFRKDLGWK-WIHEPKGYANANFCAGACPYLWSSDT-----QHSRVLSLYNTINPEASAS-PCCV--SQDLEPLTILYIGKTPKI--EQLSNMIVKSCCKCS
52		TGFβ3			CCVRPLYIDFRDLGWK-WIHEPKGYANFCGSGPCPYLRSDT-----THSTVLGLYNTLNPEASAS-PCCV--PQDLEPLTILYVGRTPKV--EQLSNMIVKSCCKCS
53		INH8A			CKKOFFVSFK-DIGWQDWI-IAPSGYHANYCEGECPSHLAG-TSGSSLSFHSVTINHYMRGHSFANLKSCCV--PTKLRPMMLYDDGQNI--KKDIQNMIVEECGCS
54		INH8B			CCRQOFFIDFR-LIGWQDWI-IAPTGYGNYCEGSCPAYLAG-VPGSASSFHTAVNQYMRGLNP-GTVNSCCI--PTKLSTMSMLYDDEYNIV-KRDVPNMIVEECGCA
55		NODAL			CRRVKFQVDEN-LIGWQDWI-IYKQYNAIRCEGECNPVGEFHPT-----NHAYTOSLLKRYQPHR-VPSTCCA--PVKTKPLSMLYDNGR--VLEHKKDMIVEECGCL
56		BMP2			CKRHPLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-K-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
57		BMP4			CRRHSLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
58		DPP			CRRHSLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
59		BMP5			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
60		BMP6			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
61		BMP7			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
62		BMP8			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
63		60A			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
64		BMP3			CARRYLVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
65		VG1			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
66		GDF1			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
67		GDF3			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
68		DORSIN			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
69		INHα			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
70		MIS			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
71		GDF9			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
72		GDNF			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR
73		NTN			CKKHLYVDFS-DVGWQDWI-IAPPGYHAFYCHGECFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYDENEKWLK-NYQDMVVEEGCGR

FIGURE 16

1	ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC
	TACCGACGTC	CTTCTGAAGC	CTAGGACACA	GACGACGAGG	ACAGGAACGT	GGGCTCGGAG
61	GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG
	CCGACCCAGG	AACTAGAAGT	TCTCCGAAGA	CACCGTCTAT	TCGAGAGTAA	ACCCTTCTAC
				↓		
121	GCAGAGACTA	GAGGGACCTG	GACGCCCCAT	CAGGGTAAGA	ATTCCTGGGG	GCCTCCCGAC
	CGTCTCTGAT	CTCCCTGGAC	CTGCGGGGTA	GTCCCATTCT	TAAGGACCCC	CGGAGGGCTG
181	TCCCCAATTC	CTTCTCTCAA	AGCCCTCACT	TTGCCTTACA	ATCCTACTCT	ACCTTGCACT
	AGGGGTAAAG	GAAGAGAGTT	TCGGGAGTGA	AACGGAATGT	TAGGATGAGA	TGGAACGTGA
	↓					
241	AGGTAACAAC	CATGTCCGTC	TTCCAAGAGC	CTTGGCTGGT	TCATGCCGAC	TGTGGAGCCT
	TCCATTGTTG	GTACAGGCAG	AAGGTTCTCG	GAACCGACCA	AGTACGGCTG	ACACCTCGGA
301	GACCCTACCA	GTGGCTGAGC	TGGGCCTGGG	CTATGCCTCG	GAGGAGAAGG	TCATCTTCCG
	CTGGGATGGT	CACCGACTCG	ACCCGGACCC	GATACGGAGC	CTCCTCTTCC	AGTAGAAGGC
361	ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGC	CCGTACCCAG	CACAGTCTGG	TACTGGCCCCG
	TATGACACGA	CCGTCGACAG	GGGTCTCTCCG	GGCATGGGTC	GTGTCAGACC	ATGACCGGGC
421	GCTTCGAGGG	CGGGGTCGAG	CCCATGGCCG	ACCCTGCTGC	CAGCCCACCA	GCTATGCTGA
	CGAAGCTCCC	GCCCCAGCTC	GGGTACCGGC	TGGGACGACG	GTCGGGTGGT	CGATACGACT
481	TGTGACCTTC	CTTGATGATC	AGCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCTGCAGC
	ACACTGGAAG	GAAGTACTAG	TCGTGGTAAC	CGTCGTCGAC	GGAGTCGAGA	GTGACGTCG
541	TTGTGGCTGT	GGTGGCTGAA	GGAGGCCAGT	CTGGTGTCTC	AGAATCACAA	GCATGAGACA
	AACACCGACA	CCACCGACTT	CCTCCGGTCA	GACCACAGAG	TCTTAGTGTT	CGTACTCTGT
601	GGCTGGGCTT	TGAAAGGCTC	AGGTGACATT	ACTAGAAATT	TGCATAGGTA	AAGATAAGAA
	CCGACCCGAA	ACTTTCCGAG	TCCACTGTAA	TGATCTTTAA	ACGTATCCAT	TTCTATTCTT
661	GGGAAAGGAC	CAGGGGTTTT	TTGTTTCTTT	CTTTGCTTGC	TTGTTAGTTT	TTTTTTTTTTT
	CCCTTTCCTG	GTCCCCAAAA	AACAAAGAAA	GAAACGAACG	AACAATCAAA	AAAAAAAAAAA
721	TTT					
	AAA					

Figure 17A

1	ATGGCTGCAG	GAAGACTTCG	GATCCTGTGT	CTGCTGCTCC	TGTCCTTGCA	CCCGAGCCTC
	TACCGACGTC	CTTCTGAAGC	CTAGGACACA	GACGACGAGG	ACAGGAACGT	GGGCTCGGAG
1	M A A G	R L R	I L C	L L L L	S L H	P S L
61	GGCTGGGTCC	TTGATCTTCA	AGAGGCTTCT	GTGGCAGATA	AGCTCTCATT	TGGGAAGATG
	CCGACCCAGG	AACTAGAAGT	TCTCCGAAGA	CACCGTCTAT	TCGAGAGTAA	ACCCTTCTAC
21	G W V / L	D L Q	E A S	V A D K	L S F	G K M
				↓		
121	GCAGAGACTA	GAGGGACCTG	GACGCCCCAT	CAGGGTAACA	ACCATGTCCG	TCTTCCAAGA
	CGTCTCTGAT	CTCCCTGGAC	CTGCGGGGTA	GTCCCATTGT	TGGTACAGGC	AGAAGGTTCT
41	A E T R	G T W	T P H	Q G N N	H V R	L P R
181	GCCTTGCGTG	GTTTCATGCCG	ACTGTGGAGC	CTGACCCCTAC	CAGTGGCTGA	GCTGGGCGCTG
	CGGAACCGAC	CAAGTACGGC	TGACACCTCG	GACTGGGATG	GTCACCGACT	CGACCCGGAC
61	A L A G	S C R	L W S	L T L P	V A E	L G L
241	GGCTATGCCT	CGGAGGAGAA	GGTCATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG
	CCGATACGGA	GCCTCCTCTT	CCAGTAGAAG	GCTATGACAC	GACCGTCGAC	AGGGGTTCTC
81	G Y A S	E E K	V I F	R Y C A	G S C	P Q E
301	GCCCGTACCC	AGCACAGTCT	GGTACTGGCC	CGGCTTCGAG	GGCGGGGTCG	AGCCCATGGC
	CGGGCATGGG	TCGTGTCAGA	CCATGACCGG	GCCGAAGCTC	CCGCCCCAGC	TCGGGTACCG
101	A R T Q	H S L	V L A	R L R G	R G R	A H G
361	CGACCCTGCT	GCCAGCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	TCAGCACCAT
	GCTGGGACGA	CGGTCGGGTG	GTCGATACGA	CTACACTGGA	AGGAACTACT	AGTCGTGGTA
121	R P C C	Q P T	S Y A	D V T F	L D D	Q H H
421	TGGCAGCAGC	TGCCTCAGCT	CTCAGCTGCA	GCTTGTGGCT	GTGGTGGCTG	A
	ACCGTCGTCG	ACGGAGTCGA	GAGTCGACGT	CGAACACCGA	CACCACCGAC	T
141	W Q Q L	P Q L	S A A	A C G C	G G	.

Figure 17B

1	ATGGCTGCAG	GAAGACTTCG	GATCTTGTTT	CTGCTGCTCC	TGTCCTTGCA	CCTGGGCCTT
	TACCGACGTC	CTTCTGAAGC	CTAGAACAAA	GACGACGAGG	ACAGGAACGT	GGACCCGGAA
61	GGCTGGGTCC	TTGATCTTCA	AGAGGCTCCT	GCGGCAGATG	AGCTCTCATC	TGGGAAAATG
	CCGACCCAGG	AAC TAGAAGT	TCTCCGAGGA	CGCCGTCTAC	TCGAGAGTAG	ACCCTTTTAC
121	GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAAGA	ATTCTTGGGG	GCCTCCTAAC
	CGTCTCTGAC	CTTCCTGGAC	CTTCGGGGTA	GTCCCATTTCT	TAAGAACCCC	CGGAGGATTG
181	TCTACAGTTC	TTCCTCTCAA	AGCCCTCACT	TTGCCTCACA	ATCCTATTCT	ACCTTGCACT
	AGATGTCAAG	AAGGAGAGTT	TCGGGAGTGA	AACGGAGTGT	TAGGATAAGA	TGGAACGTGA
241	AGGTAACAAC	AATGTCCGCC	TTCCAAGAGC	CTTACCTGGT	TTGTGCCGGC	TGTGGAGCCT
	TCCATTGTTG	TTACAGGCGG	AAGGTTCTCG	GAATGGACCA	AACACGGCCG	ACACCTCGGA
301	GACCCTACCA	GTGGCTGAGC	TTGGCCTGGG	CTATGCCTCA	GAGGAGAAGA	TTATCTTCCG
	CTGGGATGGT	CACCGACTCG	AACCGGACCC	GATACGGAGT	CTCCTCTTCT	AATAGAAGGC
361	ATACTGTGCT	GGCAGCTGTC	CCCAAGAGGT	CCGTACCCAG	CACAGTCTGG	TGCTGGCCCG
	TATGACACGA	CCGTCGACAG	GGGTTCTCCA	GGCATGGGTC	GTGTCAGACC	ACGACCGGGC
421	TCTTCGAGGG	CAGGGTCGAG	CTCATGGCAG	ACCTTGCTGC	CAGCCCACCA	GCTATGCTGA
	AGAAGCTCCC	GTCCCAGCTC	GAGTACCGTC	TGGAACGACG	GTCGGGTGGT	CGATACGACT
481	TGTGACCTTC	CTTGATGACC	ACCACCATTG	GCAGCAGCTG	CCTCAGCTCT	CAGCCGCAGC
	AACTGGAAG	GAAC TACTGG	TGGTGGTAAC	CGTCGTCGAC	GGAGTCGAGA	GTCGGCGTCG
541	TTGTGGCTGT	GGTGGCTGA				
	AACACCGACA	CCACCGACT				

Figure 18A

1	ATGGCTGCAG	GAAGACTTCG	GATCTTGTTT	CTGCTGCTCC	TGTCCTTGCA	CCTGGGCCTT
	TACCGACGTC	CTTCTGAAGC	CTAGAACAAA	GACGACGAGG	ACAGGAAACGT	GGACCCGGAA
1	M A A G	R L R	I L F	L L L L	S L H	L G L
61	GGCTGGGTCC	TTGATCTTCA	AGAGGCTCCT	GCGGCAGATG	AGCTCTCATC	TGGGAAAATG
	CCGACCCAGG	AACTAGAAGT	TCTCCGAGGA	CGCCGTCTAC	TCGAGAGTAG	ACCCTTTTAC
21	G W V L	D L Q	E A P	A A D E	L S S	G K M
121	GCAGAGACTG	GAAGGACCTG	GAAGCCCCAT	CAGGGTAACA	ACAATGTCCG	CCTTCCAAGA
	CGTCTCTGAC	CTTCCTGGAC	CTTCGGGGTA	GTCCCATTTGT	TGTTACAGGC	GGAAGGTTCT
41	A E T G	R T W	K P H	Q G N N	N V R	L P R
181	GCCTTACCTG	GTTTGTGCCG	GCTGTGGAGC	CTGACCCTAC	CAGTGGCTGA	GCTTGGCCTG
	CGGAATGGAC	CAAACACGGC	CGACACCTCG	GACTGGGATG	GTCACCGACT	CGAACCGGAC
61	A L P G	L C R	L W S	L T L P	V A E	L G L
241	GGCTATGCCT	CAGAGGAGAA	GATTATCTTC	CGATACTGTG	CTGGCAGCTG	TCCCCAAGAG
	CCGATACGGA	GTCTCCTCTT	CTAATAGAAG	GCTATGACAC	GACCGTCGAC	AGGGGTTCTC
81	G Y A S	E E K	I I F	R Y C A	G S C	P Q E
301	GTCCGTACCC	AGCACAGTCT	GGTGCTGGCC	CGTCTTCGAG	GGCAGGGTCG	AGCTCATGGC
	CAGGCATGGG	TCGTGTCAGA	CCACGACCGG	GCAGAAGCTC	CCGTCCCAGC	TCGAGTACCG
101	V R T Q	H S L	V L A	R L R G	Q G R	A H G
361	AGACCTTGCT	GCCAGCCAC	CAGCTATGCT	GATGTGACCT	TCCTTGATGA	CCACCACCAT
	TCTGGAACGA	CGGTCGGGTG	GTCGATACGA	CTACACTGGA	AGGAACTACT	GGTGGTGGTA
121	R P C C	Q P T	S Y A	D V T F	L D D	H H H
421	TGGCAGCAGC	TGCCTCAGCT	CTCAGCCGCA	GCTTGTGGCT	GTGGTGGCTG	A
	ACCGTCGTCG	ACGGAGTCGA	GAGTCGGCGT	CGAACACCGA	CACCACCGAC	T
141	W Q Q L	P Q L	S A A	A C G C	G G	.

Figure 18B



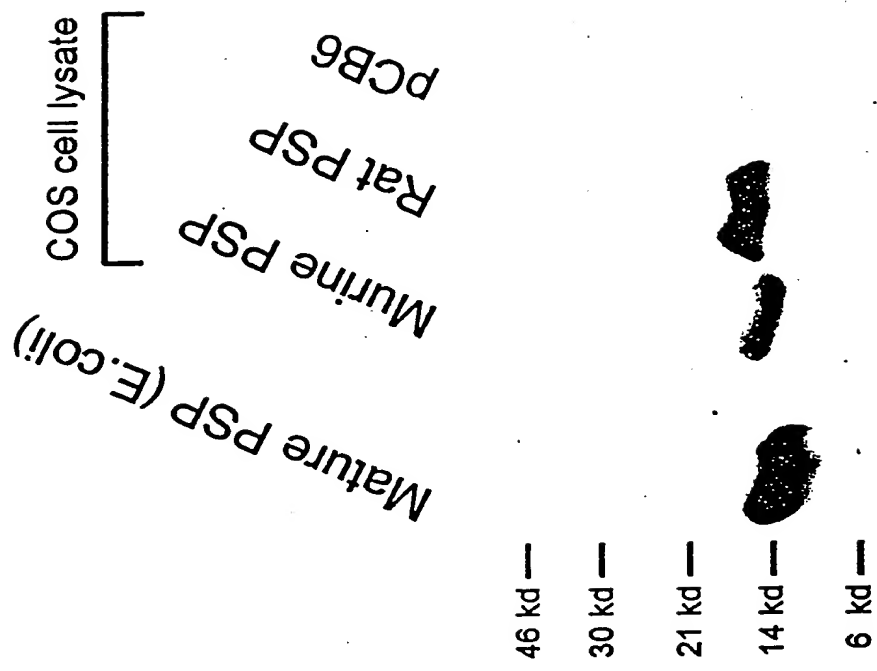


Figure 19

## FIGURE 20A

PSP/NTN (SEQ ID NO:137)

ALAGSCLWSLTLPVAELGLGYASEEKVIFRYCAGSCPQEARTQHSLVLA 50  
↓  
RLRGRGRAHGRPCCRPTAYEDEVSFLDVHSRYHTLQELSARECACV 96

## FIGURE 20B

NTN/PSP (SEQ ID NO:142)

PGARPCGLRELEVRVSELGLGYTSDETVLFRYCAGACEAAIRIYDLGLRR 50  
↓  
LRQRRRVRRERARAHPCQCPTSADVTFLDDQHHWQQLPQLSAAACGCGG 100

A high-contrast, black and white micrograph showing a dense field of small, circular, bright structures, likely representing cellular components or microorganisms. The structures are scattered across the frame, with some appearing more distinct than others. The background is dark, and the overall texture is grainy and noisy.

Figure 21a



Figure 21b

2025 RELEASE UNDER E.O. 14176

TOH labeled cells in E14 mesencephalic cultures

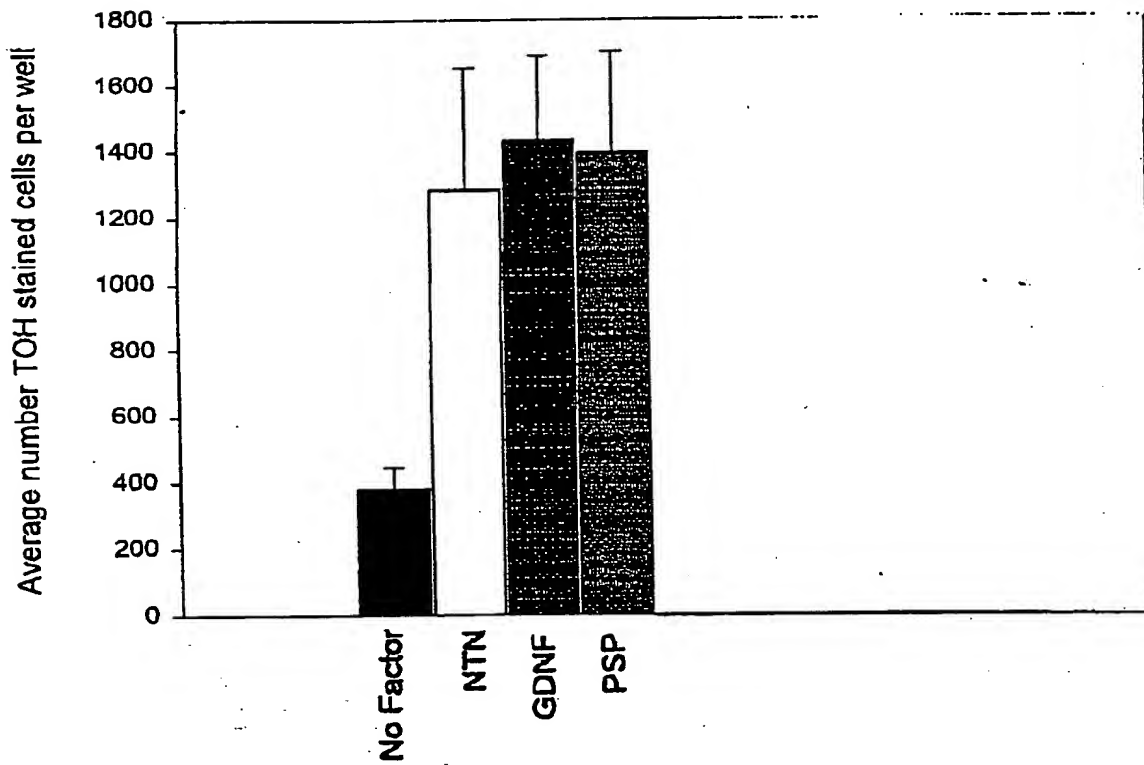


Figure 22

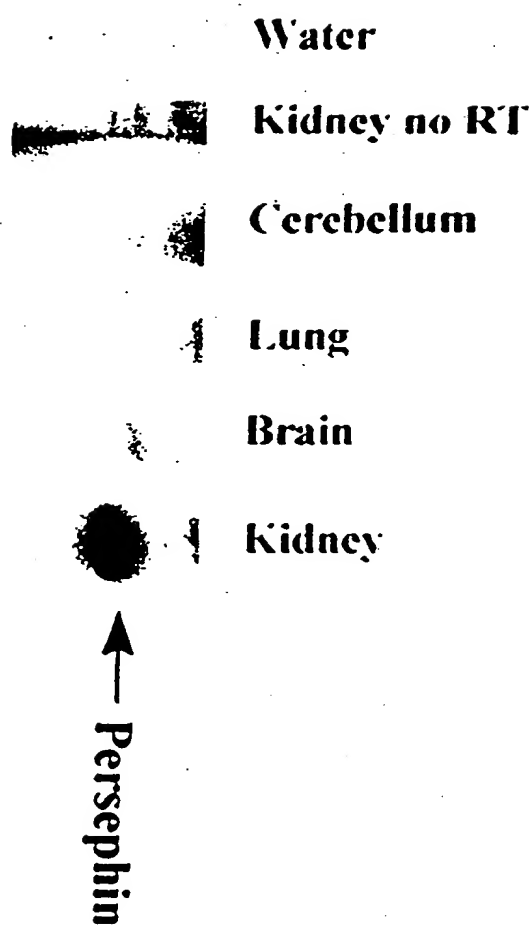


Figure 23

